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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/076,754

DATE: 03/04/2002

TIME: 15:47:23

Input Set : A:\432d3.app.txt

Output Set: N:\CRF3\03042002\J076754.raw

3 <110> APPLICANT: Alnemri, Emad S.
 5 <120> TITLE OF INVENTION: NOVEL TRAIL RECEPTORS, NUCLEIC ACIDS ENCODING SAME, AND
 6 METHODS OF USE THEREOF
 8 <130> FILE REFERENCE: 480140.432D3
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/076,754
 11 <141> CURRENT FILING DATE: 2002-02-12
 13 <160> NUMBER OF SEQ ID NOS: 6
 15 <170> SOFTWARE: PatentIn Ver. 2.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 1236
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Homo sapiens
 22 <220> FEATURE:
 23 <221> NAME/KEY: CDS
 24 <222> LOCATION: (1)..(1233)
 26 <400> SEQUENCE: 1
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 28 Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys
 29 1 5 10 15
 31 agg cac ggc cca gga ccc agg gag gcg cgg gga gcc agg cct ggg ctc 96
 32 Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Leu
 33 20 25 30
 35 cgg gtc ccc aag acc ctt gtg ctc gtt gtc gcc gcg gtc ctg ctg ttg 144
 36 Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu
 37 35 40 45
 39 gtc tca gct gag tct gct ctg atc acc caa caa gac cta gct ccc cag 192
 40 Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
 41 50 55 60
 43 cag aga gtg gcc cca caa caa aag agg tcc agc ccc tca gag gga ttg 240
 44 Gln Arg Val Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
 45 65 70 75 80
 47 tgt cca cct gga cac cat atc tca gaa gac ggt aga gat tgc atc tcc 288
 48 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
 49 85 90 95
 51 tgc aaa tat gga cag gac tat agc act cac tgg aat gac ctc ctt ttc 336
 52 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
 53 100 105 110
 55 tgc ttg cgc tgc acc agg tgt gat tca ggt gaa gtg gag cta agt ccc 384
 56 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
 57 115 120 125
 59 tgc acc acg acc aga aac aca gtg tgt cag tgc gaa gaa ggc acc ttc 432
 60 Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
 61 130 135 140

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63	cgg gaa gaa gat tct cct gag atg tgc	cg	gca aca ggg tgt	480
64	Arg Glu Glu Asp Ser Pro Glu Met Cys	Arg Lys Cys Arg Thr Gly Cys		
65	145 150	155	160	
67	ccc aga ggg atg gtc aag gtc ggt	gat tgc aca ccc tgg agt gac atc		528
68	Pro Arg Gly Met Val Lys Val Gly Asp	Cys Thr Pro Trp Ser Asp Ile		
69	165	170	175	
71	gaa tgt gtc cac aaa gaa tca ggc atc	atc ata gga gtc aca gtt gca		576
72	Glu Cys Val His Lys Glu Ser Gly Ile	Ile Ile Gly Val Thr Val Ala		
73	180	185	190	
75	gcc gta gtc ttg att gtg gct	gtg ttt gtt tgc aag tct tta ctg tgg		624
76	Ala Val Val Leu Ile Val Ala Val Phe	Val Cys Lys Ser Leu Leu Trp		
77	195	200	205	
79	aag aaa gtc ctt cct tac ctg aaa ggc	atc tgc tca ggt ggt ggt ggg		672
80	Lys Lys Val Leu Pro Tyr Leu Lys Gly	Ile Cys Ser Gly Gly Gly		
81	210	215	220	
83	gac cct gag cgt gtg gac aga agc tca	caa cga cct ggg gct gag gac		720
84	Asp Pro Glu Arg Val Asp Arg Ser Ser	Gln Arg Pro Gly Ala Glu Asp		
85	225 230	235	240	
87	aat gtc ctc aat gag atc gtg agt atc	ttg cag ccc acc cag gtc cct		768
88	Asn Val Leu Asn Glu Ile Val Ser Ile	Leu Gln Pro Thr Gln Val Pro		
89	245	250	255	
91	gag cag gaa atg gaa gtc cag gag cca	gca gag cca aca ggt gtc aac		816
92	Glu Gln Glu Met Glu Val Gln Glu Pro	Ala Glu Pro Thr Gly Val Asn		
93	260	265	270	
95	atg ttg tcc ccc ggg gag tca gag cat	ctg ctg gaa ccg gca gaa gct		864
96	Met Leu Ser Pro Gly Glu Ser Glu His	Leu Leu Glu Pro Ala Glu Ala		
97	275	280	285	
99	gaa agg tct cag agg agg ctg ctg gtt	cca gca aat gaa ggt gat		912
100	Glu Arg Ser Gln Arg Arg Leu Leu Val	Pro Ala Asn Glu Gly Asp		
101	290	295	300	
103	ccc act gag act ctg aga cag tgc ttc	gat gac ttt gca gac ttg gtg		960
104	Pro Thr Glu Thr Leu Arg Gln Cys Phe	Asp Asp Phe Ala Asp Leu Val		
105	305 310	315	320	
107	ccc ttt gac tcc tgg gag ccg ctc atg	agg aag ttg ggc ctc atg gac		1008
108	Pro Phe Asp Ser Trp Glu Pro Leu Met	Arg Lys Leu Gly Leu Met Asp		
109	325	330	335	
111	aat gag ata aag gtg gct aaa gct gag	gca gcg ggc cac agg gac acc		1056
112	Asn Glu Ile Lys Val Ala Lys Ala Glu	Ala Ala Gly His Arg Asp Thr		
113	340	345	350	
115	ttg tac acg atg ctg ata aag tgg gtc	aac aaa acc ggg cga gat gcc		1104
116	Leu Tyr Thr Met Leu Ile Lys Trp Val	Asn Lys Thr Gly Arg Asp Ala		
117	355	360	365	
119	tct gtc cac acc ctg ctg gat gcc ttg	gag acg ctg gga gag aga ctt		1152
120	Ser Val His Thr Leu Leu Asp Ala Leu	Glu Thr Leu Gly Glu Arg Leu		
121	370	375	380	
123	gcc aag cag aag att gag gac cac ttg	ttg agc tct gga aag ttc atg		1200
124	Ala Lys Gln Lys Ile Glu Asp His Leu	Leu Ser Ser Gly Lys Phe Met		
125	385 390	395	400	
127	tat cta gaa ggt aat gca gac tct gcc	atg tcc taa		1236

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128 Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser
 129 405 410
 132 <210> SEQ ID NO: 2
 133 <211> LENGTH: 411
 134 <212> TYPE: PRT
 135 <213> ORGANISM: Homo sapiens
 137 <400> SEQUENCE: 2
 138 Met Glu Gln Arg Gly Gln Asn Ala Pro Ala Ala Ser Gly Ala Arg Lys
 139 1 5 10 15
 141 Arg His Gly Pro Gly Pro Arg Glu Ala Arg Gly Ala Arg Pro Gly Leu
 142 20 25 30
 144 Arg Val Pro Lys Thr Leu Val Leu Val Val Ala Ala Val Leu Leu Leu
 145 35 40 45
 147 Val Ser Ala Glu Ser Ala Leu Ile Thr Gln Gln Asp Leu Ala Pro Gln
 148 50 55 60
 150 Gln Arg Val Ala Pro Gln Gln Lys Arg Ser Ser Pro Ser Glu Gly Leu
 151 65 70 75 80
 153 Cys Pro Pro Gly His His Ile Ser Glu Asp Gly Arg Asp Cys Ile Ser
 154 85 90 95
 156 Cys Lys Tyr Gly Gln Asp Tyr Ser Thr His Trp Asn Asp Leu Leu Phe
 157 100 105 110
 159 Cys Leu Arg Cys Thr Arg Cys Asp Ser Gly Glu Val Glu Leu Ser Pro
 160 115 120 125
 162 Cys Thr Thr Thr Arg Asn Thr Val Cys Gln Cys Glu Glu Gly Thr Phe
 163 130 135 140
 165 Arg Glu Glu Asp Ser Pro Glu Met Cys Arg Lys Cys Arg Thr Gly Cys
 166 145 150 155 160
 168 Pro Arg Gly Met Val Lys Val Gly Asp Cys Thr Pro Trp Ser Asp Ile
 169 165 170 175
 171 Glu Cys Val His Lys Glu Ser Gly Ile Ile Ile Gly Val Thr Val Ala
 172 180 185 190
 174 Ala Val Val Leu Ile Val Ala Val Phe Val Cys Lys Ser Leu Leu Trp
 175 195 200 205
 177 Lys Lys Val Leu Pro Tyr Leu Lys Gly Ile Cys Ser Gly Gly Gly
 178 210 215 220
 180 Asp Pro Glu Arg Val Asp Arg Ser Ser Gln Arg Pro Gly Ala Glu Asp
 181 225 230 235 240
 183 Asn Val Leu Asn Glu Ile Val Ser Ile Leu Gln Pro Thr Gln Val Pro
 184 245 250 255
 186 Glu Gln Glu Met Glu Val Gln Glu Pro Ala Glu Pro Thr Gly Val Asn
 187 260 265 270
 189 Met Leu Ser Pro Gly Glu Ser Glu His Leu Leu Glu Pro Ala Glu Ala
 190 275 280 285
 192 Glu Arg Ser Gln Arg Arg Arg Leu Leu Val Pro Ala Asn Glu Gly Asp
 193 290 295 300
 195 Pro Thr Glu Thr Leu Arg Gln Cys Phe Asp Asp Phe Ala Asp Leu Val
 196 305 310 315 320
 198 Pro Phe Asp Ser Trp Glu Pro Leu Met Arg Lys Leu Gly Leu Met Asp
 199 325 330 335

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Output Set: N:\CRF3\03042002\J076754.raw

201 Asn Glu Ile Lys Val Ala Lys Ala Glu Ala Ala Gly His Arg Asp Thr
 202 340 345 350
 204 Leu Tyr Thr Met Leu Ile Lys Trp Val Asn Lys Thr Gly Arg Asp Ala
 205 355 360 365
 207 Ser Val His Thr Leu Leu Asp Ala Leu Glu Thr Leu Gly Glu Arg Leu
 208 370 375 380
 210 Ala Lys Gln Lys Ile Glu Asp His Leu Leu Ser Ser Gly Lys Phe Met
 211 385 390 395 400
 213 Tyr Leu Glu Gly Asn Ala Asp Ser Ala Met Ser
 214 405 410
 217 <210> SEQ ID NO: 3
 218 <211> LENGTH: 900
 219 <212> TYPE: DNA
 220 <213> ORGANISM: Homo sapiens
 222 <220> FEATURE:
 223 <221> NAME/KEY: CDS
 224 <222> LOCATION: (1)..(897)
 226 <400> SEQUENCE: 3
 227 atg caa ggg gtg aag gag cgc ttc cta ccg tta ggg aac tct ggg gac 48
 228 Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly Asp
 229 1 5 10 15
 231 aga gcg ccc cgg ccg cct gat ggc cga ggc agg gtg cga ccc agg acc 96
 232 Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro Arg Thr
 233 20 25 30
 235 caa gac ggc gtc ggg aac cat acc atg gcc cgg atc ccc aag acc cta 144
 236 Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro Lys Thr Leu
 237 35 40 45
 239 aag ttc gtc gtc atc gtc gcg gtc ctg ctg cca gtc cta gct tac 192
 240 Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro Val Leu Ala Tyr
 241 50 55 60
 243 tct gcc acc act gcc cgg cag gag gaa gtt ccc cag cag aca gtg gcc 240
 244 Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala
 245 65 70 75 80
 247 cca cag caa cag agg cac agc ttc aag ggg gag gag tgt cca gca gga 288
 248 Pro Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly
 249 85 90 95
 251 tct cat aga tca gaa cat act gga gcc tgt aac ccg tgc aca gag ggt 336
 252 Ser His Arg Ser Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly
 253 100 105 110
 255 gtg gat tac acc aac gct tcc aac aat gaa cct tct tgc ttc cca tgt 384
 256 Val Asp Tyr Thr Asn Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys
 257 115 120 125
 259 aca gtt tgt aaa tca gat caa aaa cat aaa agt tcc tgc acc atg acc 432
 260 Thr Val Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr
 261 130 135 140
 263 aga gac aca gtg tgt cag tgt aaa gaa ggc acc ttc cgg aat gaa aac 480
 264 Arg Asp Thr Val Cys Gln Cys Lys Glu Gly Thr Phe Arg Asn Glu Asn
 265 145 150 155 160
 267 tcc cca gag atg tgc cgg aag tgt agc agg tgc cct agt ggg gaa gtc 528

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268 Ser Pro Glu Met Cys Arg Lys Cys Ser Arg Cys Pro Ser Gly Glu Val
269 165 170 175
271 caa gtc agt aat tgt acg tcc tgg gat gat atc cag tgt gtt gaa gaa 576
272 Gln Val Ser Asn Cys Thr Ser Trp Asp Asp Ile Gln Cys Val Glu Glu
273 180 185 190
275 ttt ggt gcc aat gcc act gtg gaa acc cca gct gct gaa gag aca atg 624
276 Phe Gly Ala Asn Ala Thr Val Glu Thr Pro Ala Ala Glu Glu Thr Met
277 195 200 205
279 aac acc agc ccg ggg act cct gcc cca gct gct gaa gag aca atg aac 672
280 Asn Thr Ser Pro Gly Thr Pro Ala Pro Ala Ala Glu Glu Thr Met Asn
281 210 215 220
283 acc agc cca ggg act cct gcc cca gct gct gaa gag aca atg acc acc 720
284 Thr Ser Pro Gly Thr Pro Ala Pro Ala Glu Glu Thr Met Thr Thr
285 225 230 235 240
287 agc ccg ggg act cct gcc cca gct gct gaa gag aca atg acc acc agc 768
288 Ser Pro Gly Thr Pro Ala Pro Ala Glu Glu Thr Met Thr Thr Ser
289 245 250 255
291 ccg ggg act cct gcc cca gct gct gaa gag aca atg acc acc agc ccg 816
292 Pro Gly Thr Pro Ala Pro Ala Glu Glu Thr Met Thr Thr Ser Pro
293 260 265 270
295 ggg act cct gcc tct tct cat tac ctc tca tgc acc atc gta ggg atc 864
296 Gly Thr Pro Ala Ser Ser His Tyr Leu Ser Cys Thr Ile Val Gly Ile
297 275 280 285
299 ata gtt cta att gtg ctt ctg att gtg ttt gtt tga 900
300 Ile Val Leu Ile Val Leu Leu Ile Val Phe Val
301 290 295
304 <210> SEQ ID NO: 4
305 <211> LENGTH: 299
306 <212> TYPE: PRT
307 <213> ORGANISM: Homo sapiens
309 <400> SEQUENCE: 4
310 Met Gln Gly Val Lys Glu Arg Phe Leu Pro Leu Gly Asn Ser Gly Asp
311 1 5 10 15
313 Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro Arg Thr
314 20 25 30
316 Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro Lys Thr Leu
317 35 40 45
319 Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro Val Leu Ala Tyr
320 50 55 60
322 Ser Ala Thr Thr Ala Arg Gln Glu Glu Val Pro Gln Gln Thr Val Ala
323 65 70 75 80
325 Pro Gln Gln Gln Arg His Ser Phe Lys Gly Glu Glu Cys Pro Ala Gly
326 85 90 95
328 Ser His Arg Ser Glu His Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly
329 100 105 110
331 Val Asp Tyr Thr Asn Ala Ser Asn Asn Glu Pro Ser Cys Phe Pro Cys
332 115 120 125
334 Thr Val Cys Lys Ser Asp Gln Lys His Lys Ser Ser Cys Thr Met Thr
335 130 135 140

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/076,754

DATE: 03/04/2002

TIME: 15:47:24

Input Set : A:\432d3.app.txt

Output Set: N:\CRF3\03042002\J076754.raw

L:10 M:270 C: Current Application Number differs, Wrong Format